

FIG. 1A

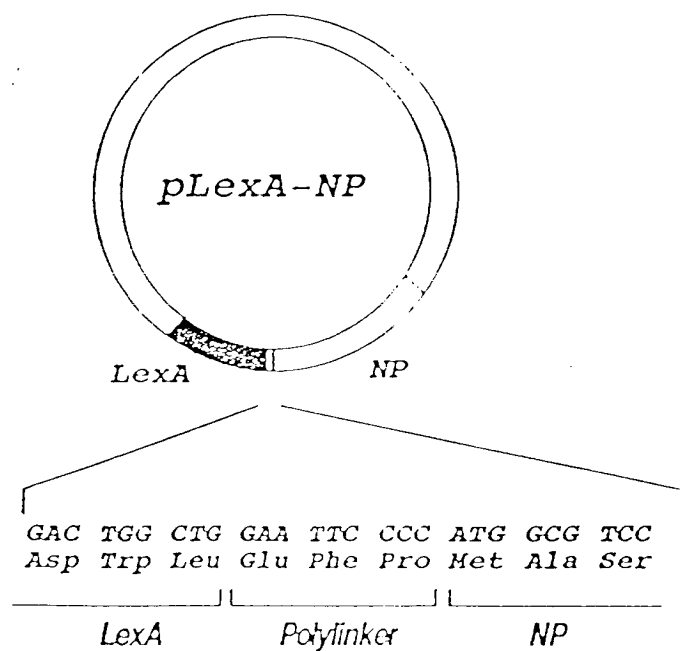


FIG. 1B

20 40 60
 CTAACCTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAATATGA CCACCCCAGG
 M T T P G>

80 100 120
 AAAAGAGAAC TTTCGCCTGA AAAGTTACAA GAACAAATCT CTGAATCCCG ATGAGATGCG
 K E N F R L K S Y K N K S L N P D E M R>

140 160 180
 CAGGAGGAGG GAGGAAGAAG GACTGCAGTT ACGAAAGCAG AAAAGAGAAG AGCAGTTATT
 F R R E E E G L Q L R K Q K R E E Q L F>

200 220 240
 CAAGCGGAGA AATGTTGCTA CAGCAGAAGA AGAAACAGAA GAAGAAGTTA TGTCAGATGG
 K R R N V A T A E E E T E E E V M S D G>

260 280 300
 AGGCTTTCAT GAGGCTCAGA TTAGTAACAT GGAGATGGCA CCAGGTGGTG TCATCACTTC
 G F H E A Q I S N M E M A P G G V I T S>

320 340 360
 TGACATGATT GAGATGATAT TTTCCAAAAG CCCAGAGCAA CAGCTTTCAG CAACACAGAA
 D M I E M I F S K S P E Q Q L S A T Q F>

380 400 420
 ATTCAGGAAG CTGCTTTCAA AAGAACCTAA CCCTCCTATT GATGAAGTTA TCAGCACACC
 F R K L L S K E P N P P I D E V I S T P>

440 460 480
 AGGAGTAGTG GCCAGGTTTG TGGAGTTCCT CAAACGAAAA GAGAATTGTT CACTGCAGTT
 G V V A R F V E F L K R F E N C S L Q F>

500 520 540
 TGAATCAGCT TGGGTACTGA CAAATATTGC TTCAGGAAAT TCTCTTCAGA CCCGAATTGT
 E S A W V L T N I A S G N S L Q T R I V>

560 580 600
 GATTCAGGCA AGAGCTGTGC CCATCTTCAT AGAGTTGCTC AGCTCAGAGT TTGAAGATGT
 I Q A R A V P I F I E L L S S E F E D V>

620 640 660
 CCAGGAACAG GCAGTCTGGG CTCTTGGCAA CATTGCTGCA GATAGTACCA TGTGCAGGGA
 Q E Q A V W A L G N I A C D S T M C R D>

680 700 720
 CTATGTCTTA GACTGCAATA TCCTTCCGCC TCTTTTGCAG TTATTTTCAA AGCAAAACCG
 Y V L D C N I L P P L L C L F S K Q N F>

740 760 780
 CCTGACCATC ACCCGGAATG CAGTATGGGC TTTGTCTAAT CTCTGTAGAG GGAAAAGTCC
 L T M T R N A V W A L S F L C E G K S P>

FIG. 2A

800 820 840
 ACCTCCAGAA TTTGCAAAGG TTTCTCCATG TCTGAATGTG CT'TTCCCTGAT TGCTGT'TTTCF
 P P E F A K V S P C L N V L S W L L F V>

860 880 900
 CAGTGACACT GATGTACTGG CTGATGCCTG CTGGGCCCTG TCATATCTAT CAGATGGAC C
 S D T D V L A D A C W A L S Y L S D G P>

920 940 960
 CAATGATAAA ATTCAAGCGG TCATCGATGC GGGAGTATGT AGGAGACTTG TGGAACCTGCT
 N D K I Q A V I D A G V C R R L V E L L>

980 1000 1020
 GATGCATAAT GATTATAAAG TGGTTTCTCC TGCTTTGCGA GCTGTGGGAA ACATTGTCAC
 M H N D Y K V V S P A L R A V G N I V T>

1040 1060 1080
 AGGGGATGAT ATTCAGACAC AGGTAATTCT GAATTGCTCA GCTCTGCAGA GTTTATTGCA
 G D D I Q T Q V I L N C S A L Q S L L H>

1100 1120 1140
 TTTGCTGAGT AGCCCAAAGG AATCTATCAA AAAGSAAGCA TGTGAGACGA TATCTAATAT
 L L S S P K E S I K K E A C W T I S N I>

1160 1180 1200
 TACAGCTGGA AATAGGGCAC AGATCCAGAC TGTGATAGAT GCCAACATTT TCCCAGCCCT
 T A G N R A Q I Q T V I D A N I F P A L>

1220 1240 1260
 CATTAGTATT TTACAAACTG CTGAATTTTCG GACAAGAAAA GAAGCAAGCTT GGGCCATCAC
 I S I L Q T A E F R T R K E A A W A I T>

1280 1300 1320
 AAATGCAACT TCTGGAGGAT CAGCTGAACA GATCAAGTAC CTAGTAGAAC TGGGTGTGAT
 N A T S G G S A E Q I K Y L V E L G C I>

1340 1360 1380
 CAAGCCGCTC TGTGATCTCC TCACGGTCAT GGACTCTAAG ATTGTACAGG TTGCCCTAAA
 K P L C D L L T V M D S K I V Q V A L N>

1400 1420 1440
 TGGCTTGGAA AATATCCTGA GGCTTGGAGA ACAGGAAGCC AAAAGGAACG GCACTGGCAT
 G L E N I L R L G E Q E A K E N G T G I>

1460 1480 1500
 TAACCCTTAC TGTGCTTTGA TTGAAGAAGC TTATGGTCTG GATAAAATTG AGTTCTTACA
 N P Y C A L I E E A Y G L D K I E F L Q>

1520 1540 1560
 GAGTCATGAA AACCAGGAGA TCTACCAAAA GGCCTTTGAT CTTATTGAGC ATTACTTCGG
 S H E N Q E I Y Q K A F D L I F H Y F G>

1580 1600 1620
 GACCGAGGAT GAAGACAGCA GATTTGCACC CCAGCTTGM CTTAACCAAT AGTATTACAT
 T E D E D S S I A F Q V E E N Q Q Q Y I>

FIG. 2B

1640 1660 1680
CTTCCAACAG TGTGAGGCTC CTATGGAAGG TTTCAGCTT TGAAGCAATA CTCATCTTTC
F Q Q C E A P M E G F Q L>

1700 1720 1740
ACGTACCTGT CCTCAGACCA GGCTACCCAG TCGAGTCCTC TTGTGGAGCC CACAGTCCTC

1760 1780 1800
ATGGAGCTAA CTCTCAAAT GTTTCCATA ATACTGTTTG CGCTCATTIG CTGCGCTTGC

1820 1840 1860
GCACCTGCTC TCTTACACAC ATCTGGAAAA CCTCCGGCTC TCTGTGGTGG GATACCCCTC

1880 1900 1920
TAATAAAAGG GTAACCAGAA CGGCCCACTC TCTTTTACGG AAAAATCCCT AGGCTTTGGA

1940 1960 1980
GATCCGCACT TACATTAGAG TTATGGGAAT ATACACATAT TAATGTGGCT CCCTTTTCT

2000 2020 2040
TGTGGGGGAA TAAAAGAGGA CTCCTCCTCA TTCCCTTTAA CATGGGGGAA AAAACTGACA

2060 2080 2100
TTAAAAGATG AGACTAAATC TTTATCTTGA ATTTTACACA ACTACTTACG ACAAGGAGGA

2120 2140 2160
TGTTTAGACC TGTGGGTATA CTTCAGAGTA CTTTTCATGA GTTCTCCAC AGTGAACCT

2180 2200 2220
TGGATTACCT GGTGGCTTTT TCTAGCCAGA TTGCATTAAT CCTTACTGAG ATTGGATGGT

2240 2260 2280
TTTCTTTCCT CTATTGAGCC CATTCTTCAG ATATTAAAGT TAAACCATCC ACTCCCTTAC

2300 2320 2340
CTTCAGCCTT CAGTGAATGT GCTTTCTAGT TGTCAGGAAT GCTGAAGAAT TAACACTTGT

2360 2380 2400
ACTCCTAAAT GTGATCTGG TGGGTAAGAG CAGGGCACAT TTAATTTGTT CGCTTTTGGT

2420 2440 2460
TCTCTTTGGT CTGGGACAT TTAATTTGTT CGCTTTTGGT TCTCTTTGGT CTTTTGAAT

2480 2500 2520
ACTTAGTAAT CGAAAACAT ATCTGTAAAT TTAATAAAAA AACTAAGGA CGAAAAAC

2540 2560 2580
CCTCCAATTT TCCCAATGC AATCAGTGA ACTAGGAGCT GTGTTTCTGC ATTAAAATAA

2600 2620 2640
ATGTTTCAGG CTTCCTGCTC CTGATTAAGG TCTTCATTAA AAAATTGGAG TTCCACCTAG

2660 2680 2700
GCTTTTCCCT TCTTCATTA GATATATAA CTAATCTTG AAAATTACTT TATGATTTT

FIG. 2C

2720 2740 2760
TTTCTTAGGT GCAGCTCGAT TCTAATCTTT TCATGCTGCA CACGATTGCT TTAATCGATA
2780 2800 2820
GCATCCTTAT CTGAAAGAAA TAACCATCTT CTCAACATGA CCTGCTTAAC CCAAATAAGA
2840 2860 2880
ACAGTGATCT TATAACCTCA TTGTTTCCTA ATCTATTTTA TTTCATCTCC TGCTAGTACT
2900 2920 2940
GTGCCGCTTC CCCCTCCCC CACACAAAAT AAAACAGTA TCTCGCTTCT GGCTCATTCT

FIG. 2D

1
MTTPGKENFRLEK
1: 111
MDNGTDSSTS K F V P E Y R R T
58

NPI-1
SRP1
13
SYKNKS-LNPDVMMRRRREEEGIQLEKLKREEQLFKRRNVVTAEETE
11111 1111 11111.1 1111 1111.1 111 1.1.1.1
SRP1
NFKNKG R F S A D E L R R R D T Q Q V E L R K A K R D E A L A K R R N F I P P T D G A D
105
59
E E V M S D G G F H E A Q I S N M E M A P G G V I T S D M I E M I F S K S P E O Q L S A T Q K
NPI-1
.1 .111 .1 111. 111.1 111.1 111.1 111.1 111.1 111.1
SRP1
S D E E D E S S V S A D Q Q F Y S Q L Q Q --- E L P Q M T Q Q L N S D D M Q E Q L S A T V K
150
106
FRKLLSKEPDPPIDE-VISTPGVVARVEFLKR-KENC SLQFESA W V
111:111.1. 1111 1: :111:1:111: : : 11:1:11.
SRP1
FRQILSREHRFPID--VVIQAGVVPRLVEFMRE-NQPEMLQLEAAWA
192
151
LTNIASGNSLQTRI--VIQARAV-PIFIELLSS-ESEDVQE-QAVWA
NPI-1
111111.1 11: : 1: 11 11:11 : .1 :1:1 11:11
SRP1
LTNIASGTS A Q T K V --- V V D A D A V - P L F I Q L L Y T - G S V E V K E - Q A I W A
235
193
LGNIAGDSTMC RDY--VLDCN IL-PPLLQLFSKQNRLTMTR-NAVWA
NPI-1
111:1111.111 1111 : 1:1 11: 1: : :1 .1:1
SRP1
LGNVAGDSTDYRDY--VLQCNAM-EPI LGLFNS-NKPSLIR-TATWT
277
236
LSNLCRGKSPPEF--AKVSPCL-NVLSWLLFV-SDTDVLA-DACWA
NPI-1
1111111.1.1. : 11. 1 .1: 1: : 11:1. 1111
SRP1
LSNLCRGKKPQPDW--SVVSQAL-PTLAKLIYS-MDTETLV-DACWA
318
278
LSYLS DGPNDKIQA---VIDAEYVET-VELLMH-NDYKVVS-PALRA
NPI-1
:111111:111 111. . 1111 1 : . 1 : 1111
SRP1
ISYLS DGPQEAIQA---VIDVRIPKRLVELLSH-ESTLVQT-PALRA
360
319
VGNIVTGDDIQTQV---ILNCSALQSLHL LSS-PKESIKK-EACWT
NPI-1
111111:1:111 :1:1 .1:1 111 111:111 1111
SRP1
VGNIVTGNDLQTQV---VINAGVLPALRL LSS-PKENIKK-EACWT
402
361
ISNITAGNRAIQT---VIDANIFPALISILQT-AEFRTK-EA AWA
NPI-1
1111111 .111: 11111:1:1:1. 11:1:1 11 11
SRP1
ISNITAGNTEQIQA---VIDANLIPPLVKLLEV-AEYKTKK-EACWA
445
403
ITNATSGG--SAEQIKYLVELGDIKPLCDLLTV-MDSKIVQ-VALNG
NPI-1
1:11:111 : : 1:11. 1111111:1:1:1: 1:1:1: 1:1:1: :
SRP1
ISNASSGGLQRPDIIRYLV SQGDIKPLCDLLEI-ADNR IIE-VTLDA
490
406
LENILRLGEQEA KRNGTG INPYCALIEEAYGLDKIEFL-LSHENQEI
NPI-1
111111:1:1. . .1.11 111.1 1:11 1 :1:1:1
SRP1
LENILKMG EADKEARGLNINENAD FIEKAGGMEKI-FNCQQQNENDKI
491
YQKAFDLIEHYFGTEDE--I S S I A P Q V D L N Q Q Q Y I F Q Q C E A P M E G F Q L
NPI-1
1:1:1:1:1 111.1:1: 1:1:11 .1
SRP1
YEKAYKI I E T Y F G E E D A V D E T M A P Q H A G N T E F G S N V N Q Q F N E N

Repeat element Consensuses:

Repeat element Consensuses:
 ARM: L+NLS*+***N+---ALL*GGL-PALV+LL*S--+E*+L*~*AA*
 A I I I I
 V V V V V

NP1-1
45BP1: LSN1*5G***QFQ---*VV1*AGV*FPLV-LL*G---*E*K4E-ACGA
 1 V A

FIG. 3

Pol/NP:

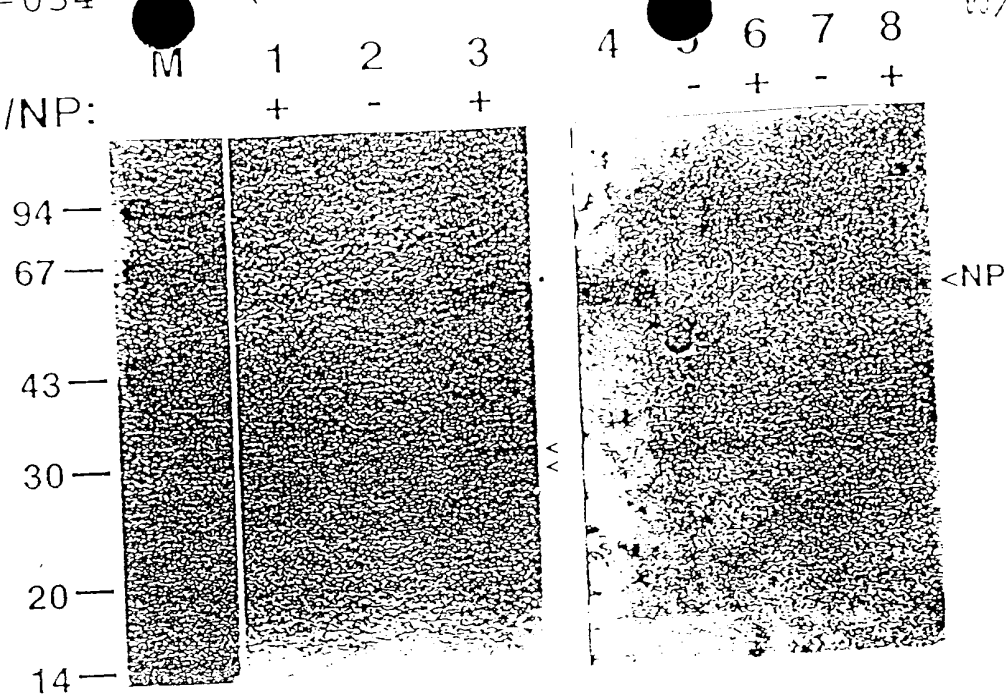


FIG. 4

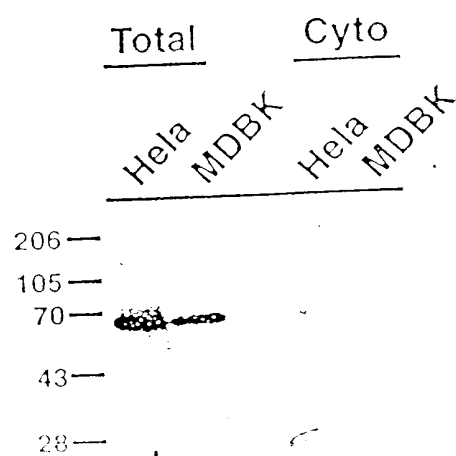


FIG. 5

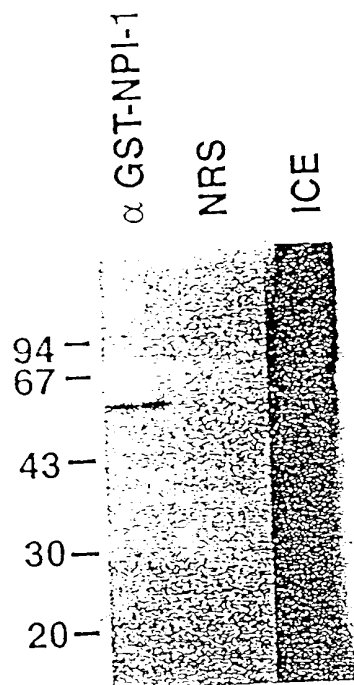


FIG. 6

20 40 60
GGAGGCACCG AAGGGCAGCG CCGAGTCGGA GGGGGCGAAG ATTGACGCCA GTAAGAACGA
80 100 120
GGAGGATGAA GGCCATTCAA ACTCCTCCCC ACGACACTCT GAAGCAGCGA CGGCACAGCG
140 160
GGAAGAATGG AAAATGTTTA TAGGAGGCCT TAGCTGGGAC ACTACAAAGA

FIG. 7

20 40 60
 GAGGTCAATG TGGAGCTGAG GAAAGCTAAG AAGGATGACC AGATGCTGAA GAGGAGAAAT
 E V N V E L F K A K F D D Q M L E F F N>

80 100 120
 GTAAGCTCAT TTCCTGATGA TGCTACTTCT CCGCTGCAGG AAAACCGCAA CAACCAGGGC
 V S S F P D D A T S P L Q E N R N N Q G>

140 160 180
 ACTGTAAATT GGTCTGTTGA TGACATTGTC AAAGGCATAA ATAGCAGCAA TGTGGAAAAT
 T V N W S V D D I V K G I N S S N V E N>

200 220 240
 CAGCTCCAAG CTACTCAAGC TGCCAGGAAA CTACTTTCCA GAGAAAAACA GCCCCCATA
 Q L Q A T Q A A R K L L S R E K Q P P I>

260 280 300
 GACAACATAA TCCGGGCTGG TTTGATTCCG AAATTGTGT CCTTCTTGGG CAGAACTGAT
 D N I I R A G L I P K F V S F L G R T D>

320 340 360
 TGTAAGTCCCA TTCAGTTTGA ATCTGCTTGG GCACTCACTA ACATTGCTTC TGGGAJATCA
 C S P I Q F E S A W A L T N I A S G T S>

380 400 420
 GAACAAACCA AGGCTGTG3T AGATGGAGGT GCCATCCCAG CATTCAATTC TCTGTTGGCA
 E Q T K A V V D G G A I P A F I S L L A>

440 460 480
 TCTCCCCATG CTCACATCAG TGAACAAGCT GTCTGG3CTC TAGGAAACAT TGCAGGTGAT
 S P H A H I S E Q A V W A L G N I A G D>

500 520 540
 GGCTCAGTGT TCCGAGACTT GGTATTAAAG TACG3TGCAG TTGACCCACT GTTGG3CTCTC
 G S V F F D L V I K Y G A V D F L I A L>

560 580 600
 CTTGCAGTTC CTGATATGTC ATCTTTAGCA TGTGGCTACT TACGTAATCT TACCTGGACA
 L A V P D M S S L A C G Y L R N L T W T>

620 640 660
 CTTTCTAATC TTTGCCGCAA CAAGAATCCT GCACCCCGCA TAGATGCTGT TGAGCAGATT
 L S N L C R N K N P A P P I D A V E Q I>

680 700 720
 CTTCCTACCT TAGTTCGGCT CCTGCATCAT GATGATCCAG AAGTGTTAGC AGATACCTGC
 L P T L V E L L H H D D P E V L A D T C>

740 760 780
 TGGGCTATTT CTACCTTAC TGATG3TCCA AATGAACGAA TTGGCATGGT GGTGAAAACA
 W A I S Y L T D G P N E F I C M V V K T>

FIG. 8A

800 820 840
 GGAGTTGTGC CCCAACTTGT GAAGCTTCTA GGAGCTTCTG AATIGCCAAT TGTGACTCCT
 G V V P Q L V F L L G A S E L P I V T P>

860 880 900
 GCCCTAAGAG CCATAGGGAA TATTGTCACT GGTACAGATG AACAGACTCA GGTGTGATTT
 A L R A I G N I V T G T D E Q T Q V V I>

920 940 960
 GATGCAGGAG CACTCGCCGT CTTTCCCAGC CTGCTCACCA ACCCCAAAAC TAACATTCAG
 D A G A L A V F P S L L T N P K T N I Q>

980 1000 1020
 AAGGAAGCTA CGTGGACAAT GTCAAACATC ACAGCCGGCC GCCAGGACCA GATACAGCAA
 K E A T W T M S N I T A G R Q D Q I Q Q>

1040 1060 1080
 GTTGTGAATC ATGGATTAGT CCCATTCTTT GTGAGTGTTC TCTCTAAGGC AGATTTTAAAG
 V V N H G L V P F L V S V L S K A D F K>

1100 1120 1140
 ACACAAAAGG AAGCTGTGTG GGCCCTGACC AACTATACCA GTGGTGGAAC AGTTGAACAG
 T Q K E A V W A V T N Y T S G G T V E Q>

1160 1180 1200
 ATTGTGTACC TTGTTCACTG TGGCATAATA GAACCGTTGA TGAACCTCTT AACTGCAAAA
 I V Y L V H C G I I E P L M N L L T A F>

1220 1240 1260
 GATACCAAGA TTATTCTGCT TATCCTGGAT GCCATTTCAG ATATCTTTCA GGCTGCTGAG
 D T K I I L V I L D A I S N I F Q A A E>

1280 1300 1320
 AAAGTAGGTT AAAGTAGGTT CCCGTCTTCA CAGATTCAAG AACAAAGGAA AAGACAGTAC
 K L G E T S C P S S Q I Q E Q G K R Q Y>

1340 1360 1380
 AGAAATGAGG CGTCCGAGGC GTGCGAGAAT AGAGAACTT AGTATAATGA TTGAAGAATG
 F N E A S E A S Q N R E T>

1400 1420 1440
 TGGAGGCTTA GACAAAATTG AAGCTCTACA AAACCATGAA AATGAGTCTG TGTATAAGGC
 T T C G T T A A G C T T A A T T G A G A G T A T T T C T C T G T A G A G A A G A G G A A G A T C A A A C G T T G T

1460 1480 1500
 ACCAGAACT ACCTCTGAG GCTACACTTT CCAAGTTCAG GATGGGGCTC CTGGGACCTT

1520 1540 1560
 TAACTTTTAG ATCATGTAGC TGAGACATAA ATTTGTTGTG TACTACGTTT GGTATTTTGT

1580 1600 1620
 CTTATTCTTT CTCTACTTAC AACTCTTTCT TAAATTTGCT TTGTTACTTT AGCACTTTT

1640 1660 1680

FIG. 8B

1700 1720 1740
ACACTGAAAC TATACTTGAA CAGTTCCAAC TGTACATACA TACTGTATGA AGCTTGTCCT
1760 1780 1800
CTGACTAGGT TTCTAATTTC TATGTGGAAT TTCTATCTTT GCAGATCTT GTAAATAAAC
1820
ATTCAAGTCC ACCCTTTTCT TGACTTC

FIG. 8C

20 40 60
 GAGCGACCAA GAGGGTGTTC GACTGCTAGA GCGGACGAGA AGCGTGCCTA AATCAAGGA
 80 100 120
 ACTTGTTTCT TCAAGCTCTT CTGGCAGTGA TTCTGACAGT GAGGTTGACA AAAAGTTAAG
 140 160 180
 CAGGAAAAAG CAAGTTGCTC CAGAAAAACC TGTAAAGAAA CAAAAGACAG GTGAGACTTC
 200 220 240
 GAGAGCCCTG TCATCTTCTA AACAGAGCAG CAGCAGCAGA GATGATAACA TGTTTCAGAT
 TGGGAAAATG AGGTCAGTT

FIG. 9

20 40 60
TGTCCACTGT GGCTTTGAGC ATCCGTCAGA AGTCCAGCAT GAGTGCATCC CTCAGGCCAT
80 100 120
TCTGGGAATG GATGTCCTGT GCCAGGCCAA GTCCGGCATG GGAAAGACAG CAGTGTTTGT
140 160 180
CTTGGCCACA CTGCAACAGC TGGAGCCAGT TACTGGGCAG GTCTCTGTAC TGGTGATGTG
200 220
TCACACTCGG GAGTTGGCTT TTCAGATCAG CAAGGAATAT G

FIG. 10

20 40 60
ATTTGTAAAC CCCGGAGCGA GGTCTTGCTT ACCCGAGGCC GCTGCTGTGC GGAGACCCCC
80 100 120
GGGTGAAGCC ACCGTCATCA TGTCTGACCA GGAGGCAAAA CCTTCAACTG AGGACTTGGG
140 160 180
GGATAAGAAG GAAGGTGAAT ATATTAACT CAAAGTCATT GGACAGGATA GCAGTGAGAT
200 220 240
TCACTTCAAA GTGAAAATGA CAACACATCT CAAGAACTC AAAGAATCAT ACTGTCAAAG
260 280 300
ACAGGGTGT CCAATGAATT CACTCAGGTT TCTCTTTGAG GGTGAGAGAA TTGCTGATAA
320 340 360
TCATACTCCA AAAGAACTGG GAATGGAGGA AGAAGTTGTG ATTGAAGTTT ATCAGGAACA
AACGGGGGGT CA

FIG. 11

- 90

FIG. 12A

1441 GTAGCCATACCTAATAGACCTCCTGATGCTGTACTTACAGATACCACCTCTCTTAATCAGGCTGCTTTGTACCGCCTCAG 1520
V A I P N R P P D A V L T D T T S L N Q A A L Y R L S 507

1521 TGGAGACCGGAATCCCTTACACATTGATCCTAACTTTGCTAGTCTAGCAGGTTTGGACAAGCCCATATTACATGGATTAT 1600
G D R N P L H I D P N F A S L A G F D K P I L H G L 532

1601 GTACATTGGATTCTCTGCCAGGCGTGTGTTACAGCAGTTTGCAGATAATGATGTGTCAAGATTCAAGGCAGTTAAGGCT 1680
C T F G F S A R R V L Q Q F A D N D V S F F K A V K A 560

1681 CGTTTTGCAAAACCAGTATATCCAGGACAACTCTACAACTGAGATGTGGAAGGAAGCAACAGAATTCATTTTCAAAC 1760
R F A K P V Y P G Q T L Q T E M W K E G N R I H F Q T 587

1761 CAAGGTCCAAGAACTGGAGACATTGTCATTTCAAATGCATATGTGGATCTTGCACCAACATCTGGTACTTCAGCTAAGA 1840
K V Q E T G D I V I S N A Y V D L A P T S G T S A K 613

1841 CACCCTCTGAGGGCGGGAAGCTTCAGAGTACCTTTGTATTGAGGAAATAGGACGCCGCTAAAGGATATTGGGCCTGAG 1920
T P S E G G K L Q S T F V F E E I G R R L K D I G P E 640

1941 GTGGTGAAGAAAGTAAATGCTGTATTGAGTGGCATATAACCAAAGGCGGAAATATTGGGGCTAAGTGGACTATTGACCT 2000
V V K K V N A V F E W H I T K G G N I G A K W T I D L 667

2001 GAAAAGTGGTTCTGGAAAAGTGTACCAAGGCCCTGCAAAAGGTGCTGCTGATACAACAATCATACTTTTCAGATGAAGATT 2080
K S G S G K V Y Q G P A K G A A D T T I I L S D E D 693

2081 TCATGGAGGTGGTCTCTGGCAAGCTTGACCCTCAGAAGGCATTCTTTAGTGGCAGGCTGAAGGCCAGAGGGAACATCATG 2160
F M E V V L G K L D P Q K A F F S G R L K A R G N I M 720

2161 CTGAGCCAGAACTTCAGATGATTCTTAAAGACTACGCCAAGCTCTGAAGGGCACACTACACTATTAATAAAAAATGGAAT 2240
L S Q K L Q M I L K D Y A K L 735

2241 CATTAAATACTCTCTTACCCAAATATGCTTGATTATTCTGCAAAAGTGATTAGAACTAAGATGCAGGGGAAATTGCTTA 2320

2340 ACATTTTCAGATATCAGATAACTGCAGATTTTCATTTTCTACTAATTTTTCATGTATCATTATTTTACAAGGAATATA 2400

2401 TATAAGCTAGCACATAATATCCTTCTGTTCTTAGATCTGTATCTTCATAATAAAAAATTTTGCCCAAGTCCTGTTTCC 2480

2480 TTAGAATTTGTGATAGCATTGATAAGTTGAAAGGAAATTAATCAATAAAGGCCTTTGATACCTTTAAAAA

AAAAA

FIG. 12B

08/444994

Kb

9.5 .

7.5 .

4.4 .

2.37 .

1.35 .

0.24 .

FIG. 13

08/444994

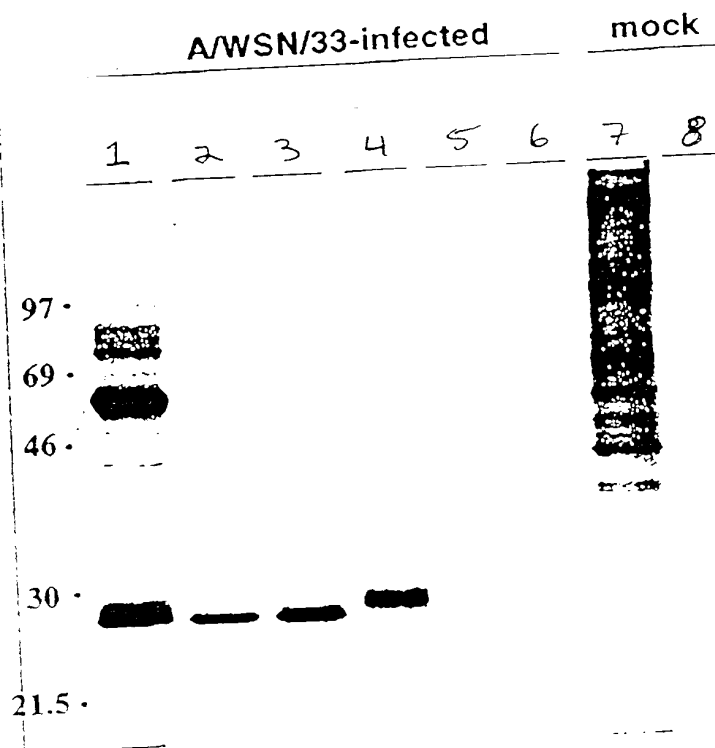


FIG. 14

08/444994

PANEL A

PANEL B

A/turkey/Oregon/71
 α - GST-
 T NS1 K5 NI GST

A/duck/Alberta/76
 α - GST-
 T NS1 K5 NI GST

NS1 →

MI
 NS1

FIG. 15A

PANEL C PANEL D PANEL E

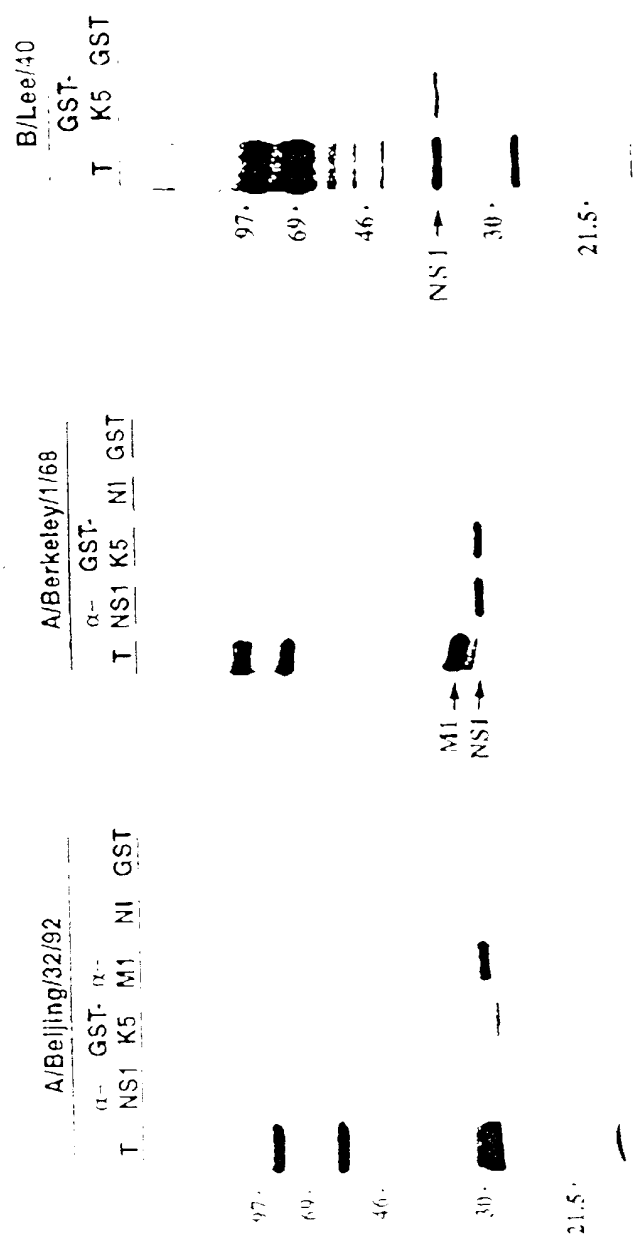


FIG. 15B